

1 1. An oligonucleotide primer, wherein said primer is capable of specifically
2 hybridizing to a DNA having the sequence of the flanking regions of a microsatellite
3 selected from the group consisting of M2_4_9, M2_2_9, M2_2_12, M2_3_11, M2_2_20,
4 M2_2_21, M2_2_22, M2_2_23, M2_2_24, M2_4_25, M2_4_26, M2_2_29, M2_2_32,
5 M2_4_32, M2_4_33, M2_4_37, M2_3_22, M2_2_36, M2_5_11, M2_2_46, and
6 M2_2_48.

1 2. The oligonucleotide primer according to claim 1, wherein the sequence of said
2 primer is selected from the group consisting of SEQ ID NOs: 1-42.

1 3. A kit for determining the number of repeat units of a microsatellite selected from
2 the group consisting of M2_4_9, M2_2_9, M2_2_12, M2_3_11, M2_2_20, M2_2_21,
3 M2_2_22, M2_2_23, M2_2_24, M2_4_25, M2_4_26, M2_2_29, M2_2_32, M2_4_32,
4 M2_4_33, M2_4_37, M2_3_22, M2_2_36, M2_5_11, M2_2_46, and M2_2_48, the kit
5 comprising a pair of oligonucleotide primers having the sequence of the flanking regions
6 of said microsatellite.

1 4. The kit according to claim 3, wherein the pair of oligonucleotide primers is
2 selected from the group consisting of

- 3 (a) SEQ ID NO: 1 and SEQ ID NO: 2,
- 4 (b) SEQ ID NO: 3 and SEQ ID NO: 4,
- 5 (c) SEQ ID NO: 5 and SEQ ID NO: 6,
- 6 (d) SEQ ID NO: 7 and SEQ ID NO: 8,
- 7 (e) SEQ ID NO: 9 and SEQ ID NO: 10,
- 8 (f) SEQ ID NO: 11 and SEQ ID NO: 12,
- 9 (g) SEQ ID NO: 13 and SEQ ID NO: 14,
- 10 (h) SEQ ID NO: 15 and SEQ ID NO: 16,
- 11 (i) SEQ ID NO: 17 and SEQ ID NO: 18,
- 12 (j) SEQ ID NO: 19 and SEQ ID NO: 20,
- 13 (k) SEQ ID NO: 21 and SEQ ID NO: 22,
- 14 (l) SEQ ID NO: 23 and SEQ ID NO: 24,
- 15 (m) SEQ ID NO: 25 and SEQ ID NO: 26,

- 16 (n) SEQ ID NO: 27 and SEQ ID NO: 28,
17 (o) SEQ ID NO: 29 and SEQ ID NO: 30,
18 (p) SEQ ID NO: 31 and SEQ ID NO: 32,
19 (q) SEQ ID NO: 33 and SEQ ID NO: 34,
20 (r) SEQ ID NO: 35 and SEQ ID NO: 36,
21 (s) SEQ ID NO: 37 and SEQ ID NO: 38,
22 (t) SEQ ID NO: 39 and SEQ ID NO: 40, and
23 (u) SEQ ID NO: 41 and SEQ ID NO: 42.

1 5. A method for determining the number of repeat units of a microsatellite, the
2 method comprising a step for determining the number of repeat units in the region of
3 which DNA can be amplified by using a pair of oligonucleotide primers selected from the
4 group consisting of,

- 5 (a) SEQ ID NO: 1 and SEQ ID NO: 2,
6 (b) SEQ ID NO: 3 and SEQ ID NO: 4,
7 (c) SEQ ID NO: 5 and SEQ ID NO: 6,
8 (d) SEQ ID NO: 7 and SEQ ID NO: 8,
9 (e) SEQ ID NO: 9 and SEQ ID NO: 10,
10 (f) SEQ ID NO: 11 and SEQ ID NO: 12,
11 (g) SEQ ID NO: 13 and SEQ ID NO: 14,
12 (h) SEQ ID NO: 15 and SEQ ID NO: 16,
13 (i) SEQ ID NO: 17 and SEQ ID NO: 18,
14 (j) SEQ ID NO: 19 and SEQ ID NO: 20,
15 (k) SEQ ID NO: 21 and SEQ ID NO: 22,
16 (l) SEQ ID NO: 23 and SEQ ID NO: 24,
17 (m) SEQ ID NO: 25 and SEQ ID NO: 26,
18 (n) SEQ ID NO: 27 and SEQ ID NO: 28,
19 (o) SEQ ID NO: 29 and SEQ ID NO: 30,
20 (p) SEQ ID NO: 31 and SEQ ID NO: 32,
21 (q) SEQ ID NO: 33 and SEQ ID NO: 34,
22 (r) SEQ ID NO: 35 and SEQ ID NO: 36,
23 (s) SEQ ID NO: 37 and SEQ ID NO: 38,

24 (t) SEQ ID NO: 39 and SEQ ID NO: 40, and

25 (u) SEQ ID NO: 41 and SEQ ID NO: 42.

- 1 6. A method for mapping of susceptibility genes for disease associated with HLA
2 class II alleles, by using a microsatellite marker selected from the group consisting of
3 M2_4_9, M2_2_9, M2_2_12, M2_3_11, M2_2_20, M2_2_21, M2_2_22, M2_2_23,
4 M2_2_24, M2_4_25, M2_4_26, M2_2_29, M2_2_32, M2_4_32, M2_4_33, M2_4_37,
5 M2_3_22, M2_2_36, M2_5_11, M2_2_46, and M2_2_48, the method comprising:
6 (a) determining the number of repeat units of said microsatellite,
7 (b) estimating the allele frequencies of patients and controls, based on said number, and
8 (c) comparing the allele frequencies of patients with those of controls.

- 1 7. The method according to claim 6, the method comprising:
2 (a) amplifying a region of microsatellite using the oligonucleotide primer capable of
3 selectively hybridizing to a DNA having a sequence of flanking regions of said
4 microsatellite,
5 (b) determining the number of repeat units of said microsatellite,
6 (c) estimating the allele frequencies of patients and controls, based on the number, and
7 (d) comparing the allele frequencies of patients with those of controls.

- 1 8. A method for genotyping of a microsatellite allele selected from the group
2 consisting of M2_4_9, M2_2_9, M2_2_12, M2_3_11, M2_2_20, M2_2_21, M2_2_22,
3 M2_2_23, M2_2_24, M2_4_25, M2_4_26, M2_2_29, M2_2_32, M2_4_32, M2_4_33,
4 M2_4_37, M2_3_22, M2_2_36, M2_5_11, M2_2_46, and M2_2_48, the method
5 comprising:
6 (a) amplifying a region of the microsatellite, and
7 (b) determining the number of repeat units of said microsatellite.

- 1 9. The method according to claim 7, wherein said amplifying is performed by using
2 the oligonucleotide primer selected from the group consisting of SEQ ID NOs: 1-42.